

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Coleman, Roger
Au-Young, Janice
Bandman, Olga
Seilhamer, Jeffrey J.
- (ii) TITLE OF INVENTION: C5a-Like Seven Transmembrane Receptor
- (iii) NUMBER OF SEQUENCES: 2
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 - (B) STREET: 3330 Hillview Avenue
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: USA
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Luther, Barbara J.
 - (B) REGISTRATION NUMBER: 33954
 - (C) REFERENCE/DOCKET NUMBER: PF-0040 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-852-0195

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1446 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: Mast Cell
 - (B) CLONE: 8118
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGCGTCTT TCTCTGCTGA GACCAATTCA ACTGACCTAC TCTCACAGCC ATGGAATGAG	60
CCCCCAGTAA TTCTCTCCAT GGTCATTCTC AGCCTTACTT TTTTACTGGG ATTGCCAGGC	120
AATGGGCTGG TGCTGTGGGT GGCTGGCCTG AAGATGCAGC GGACAGTGAA CACAATTTGG	180
TTCCTCCACC TCACCTTGGC GGACCTCCTC TGCTGCCTCT CCTTGGCCTT CTCGCTGGCT	240
CACTTGGCTC TCCAGGGACA GTGGCCCTAC GGCAGGTTCC TATGCAAGCT CATCCCCTCC	300
ATCATTGTCC TCAACATGTT TGGCAGTGTC TTCCTGCTTA CTGCCATTAG CCTGGATCGC	360
TGTCTTGTGG TATTCAAGCC AATCTGGTGT CAGAATCATC GCAATGTAGG GATGGCCTGC	420
TCTATCTGTG GATGTATCTG GGTGGTGGCT TTTGTGTTGT GCATTCTGT GTTCGTGTAC	480
CGGGAAATCT TCACTACAGA CAACCATAAT AGATGTGGCT ACAAATTTGG TCTCTCCAGC	540
TCATTAGATT ATCCAGACTT TTATGGGGAT CCACTAGAAA ACAGGTCTCT TGAAAACATT	600
GTTCAGCCGC CTGGAGAAAT GAATGATAGG TTAGATCCTT CCTCTTTCCA AACAAATGAT	660
CATCCTTGGA CAGTCCCCAC TGTCTTCCAA CCTCAAACAT TTCAAAGACC TTCTGCAGAT	720
TCACTCCCTA GGGGTTCTGC TAGGTTAACA AGTCAAAATC TGTATTCTAA TGTATTTAAA	780
CCTGCTGATG TGGTCTCACC TAAATCCCC AGTGGGTTTC CTATTGAAGA TCACGAAACC	840
AGCCCACTGG ATAACTCTGA TGCTTTTCTC TCTACTCATT TAAAGCTGTT CCCTAGCGCT	900
TCTAGCAATT CCTTCTACGA GTCTGAGCTA CCACAAGGTT TCCAGGATTA TTACAATTTA	960
GGCCAATTCA CAGATGACGA TCAAGTGCCA ACACCCCTCG TGGCAATAAC GATCACTAGG	1020
CTAGTGGTGG GTTTCCTGCT GCCCTCTGTT ATCATGATAG CCTGTTACAG CTTCATTGTC	1080
TTCCGAATGC AAAGGGGCCG CTTGCGCAAG TCTCAGAGCA AAACCTTTTCG AGTGGCCGTG	1140
GTGGTGGTGG CTGTCTTTCT TGTCTGCTGG ACTCCATACC ACATTTGGGG AGTCCTGTCA	1200
TTGCTTACTG ACCCAGAAAC TCCCTTGGGG AAAACTCTGA TGTCCTGGGA TCATGTATGC	1260
ATTGCTCTAG CATCTGCCAA TAGTTGCTTT AATCCCTTCC TTTATGCCCT CTTGGGGAAA	1320
GATTTTAGGA AGAAAGCAAG GCAGTCCATT CAGGGAATTC TGGAGGCAGC CTTCAGTGAG	1380
GAGCTCACAC GTTCCACCCA CTGTCCCTCA AACAATGTCA TTTCAGAAAG AAATAGTACA	1440
ACTGTG	1446

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Ser	Phe	Ser	Ala	Glu	Thr	Asn	Ser	Thr	Asp	Leu	Leu	Ser	Gln
1				5					10					15	
Pro	Trp	Asn	Glu	Pro	Pro	Val	Ile	Leu	Ser	Met	Val	Ile	Leu	Ser	Leu
			20					25					30		
Thr	Phe	Leu	Leu	Gly	Leu	Pro	Gly	Asn	Gly	Leu	Val	Leu	Trp	Val	Ala
		35					40					45			
Gly	Leu	Lys	Met	Gln	Arg	Thr	Val	Asn	Thr	Ile	Trp	Phe	Leu	His	Leu
	50					55					60				
Thr	Leu	Ala	Asp	Leu	Leu	Cys	Cys	Leu	Ser	Leu	Ala	Phe	Ser	Leu	Ala
	65				70					75					80
His	Leu	Ala	Leu	Gln	Gly	Gln	Trp	Pro	Tyr	Gly	Arg	Phe	Leu	Cys	Lys
				85					90					95	
Leu	Ile	Pro	Ser	Ile	Ile	Val	Leu	Asn	Met	Phe	Gly	Ser	Val	Phe	Leu
			100					105					110		
Leu	Thr	Ala	Ile	Ser	Leu	Asp	Arg	Cys	Leu	Val	Val	Phe	Lys	Pro	Ile
		115					120					125			
Trp	Cys	Gln	Asn	His	Arg	Asn	Val	Gly	Met	Ala	Cys	Ser	Ile	Cys	Gly
	130					135					140				
Cys	Ile	Trp	Val	Val	Ala	Phe	Val	Leu	Cys	Ile	Pro	Val	Phe	Val	Tyr
145					150					155					160
Arg	Glu	Ile	Phe	Thr	Thr	Asp	Asn	His	Asn	Arg	Cys	Gly	Tyr	Lys	Phe
				165					170					175	
Gly	Leu	Ser	Ser	Ser	Leu	Asp	Tyr	Pro	Asp	Phe	Tyr	Gly	Asp	Pro	Leu
			180					185					190		
Glu	Asn	Arg	Ser	Leu	Glu	Asn	Ile	Val	Gln	Pro	Pro	Gly	Glu	Met	Asn
		195					200					205			
Asp	Arg	Leu	Asp	Pro	Ser	Ser	Phe	Gln	Thr	Asn	Asp	His	Pro	Trp	Thr
	210					215					220				
Val	Pro	Thr	Val	Phe	Gln	Pro	Gln	Thr	Phe	Gln	Arg	Pro	Ser	Ala	Asp
225					230					235					240
Ser	Leu	Pro	Arg	Gly	Ser	Ala	Arg	Leu	Thr	Ser	Gln	Asn	Leu	Tyr	Ser
				245					250					255	
Asn	Val	Phe	Lys	Pro	Ala	Asp	Val	Val	Ser	Pro	Lys	Ile	Pro	Ser	Gly
			260					265					270		
Phe	Pro	Ile	Glu	Asp	His	Glu	Thr	Ser	Pro	Leu	Asp	Asn	Ser	Asp	Ala
		275					280					285			
Phe	Leu	Ser	Thr	His	Leu	Lys	Leu	Phe	Pro	Ser	Ala	Ser	Ser	Asn	Ser
	290					295					300				
Phe	Tyr	Glu	Ser	Glu	Leu	Pro	Gln	Gly	Phe	Gln	Asp	Tyr	Tyr	Asn	Leu
305					310					315					320

Gly Gln Phe Thr Asp Asp Asp Gln Val Pro Thr Pro Leu Val Ala Ile
325 330 335

Thr Ile Thr Arg Leu Val Val Gly Phe Leu Leu Pro Ser Val Ile Met
340 345 350

Ile Ala Cys Tyr Ser Phe Ile Val Phe Arg Met Gln Arg Gly Arg Phe
355 360 365

Ala Lys Ser Gln Ser Lys Thr Phe Arg Val Ala Val Val Val Val Ala
370 375 380

Val Phe Leu Val Cys Trp Thr Pro Tyr His Ile Trp Gly Val Leu Ser
385 390 395 400

Leu Leu Thr Asp Pro Glu Thr Pro Leu Gly Lys Thr Leu Met Ser Trp
405 410 415

Asp His Val Cys Ile Ala Leu Ala Ser Ala Asn Ser Cys Phe Asn Pro
420 425 430

Phe Leu Tyr Ala Leu Leu Gly Lys Asp Phe Arg Lys Lys Ala Arg Gln
435 440 445

Ser Ile Gln Gly Ile Leu Glu Ala Ala Phe Ser Glu Glu Leu Thr Arg
450 455 460

Ser Thr His Cys Pro Ser Asn Asn Val Ile Ser Glu Arg Asn Ser Thr
465 470 475 480

Thr Val